

SEQUENCE LISTING

#24/E

<110> Kauppinen, Markus
Schulein, Martin
Schnorr, Kirk
Andersen, Lene
Bjornvad, Mads

<120> Novel Mannanases

<130> 5440.204-US

<160> 55

<170> PatentIn version 3.1

<210> 1

<211> 1470

<212> DNA

<213> Bacillus sp. I633

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208

E

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 <211> 490
 <212> PRT
 <213> Bacillus

<400> 2

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Leu Ala Ser Ser Ile Leu Phe Val Ser Gly Thr Ser Thr Ala Asn Ala
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Asn Ser Gly Phe Tyr Val Ser Gly Thr Thr Leu Tyr Asp Ala Asn Gly
 N S 35 F Y V S 40 G T T L Y 45 D A N G

Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
 50 55 60

Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala Asn
 65 70 75 80

Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp Asp
 85 90 95

Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His Leu
 100 105 110

Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile Ala
 115 120 125

Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala Leu
 130 135 140

209

E

Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Phe
145 150 155 160

Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala Ile
165 170 175

Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp Ala
180 185 190

Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg Glu
195 200 205

Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His Met
210 215 220

Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile Asp
225 230 235 240

Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
245 250 255

Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr Ser
260 265 270

Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Gly
275 280 285

Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn Asn
290 295 300

Leu Thr Ala Trp Gly Asn Thr Ile Val Asn Gly Pro Tyr Gly Leu Arg
305 310 315 320

Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Gly Gly Gly Ser Asp Gly
325 330 335

Gly Thr Ser Pro Thr Thr Leu Tyr Asp Phe Glu Gly Ser Met Gln Gly
340 345 350

Trp Thr Gly Ser Ser Leu Ser Gly Gly Pro Trp Ala Val Thr Glu Trp
355 360 365

3210

E

Ser Ser Lys Gly Ser His Ser Leu Lys Ala Asp Ile Gln Leu Ser Ser
370 375 380

Asn Ser Gln His Tyr Leu His Val Ile Gln Asn Thr Ser Leu Gln Gln
385 390 395 400

Asn Ser Arg Ile Gln Ala Thr Val Lys His Ala Asn Trp Gly Ser Val
405 410 415

Gly Asn Gly Met Thr Ala Arg Leu Tyr Val Lys Thr Gly His Gly Tyr
420 425 430

Thr Trp Tyr Ser Gly Ser Phe Val Pro Ile Asn Gly Ser Ser Gly Thr
435 440 445

Thr Leu Ser Leu Asp Leu Ser Asn Val Gln Asn Leu Ser Gln Val Arg
450 455 460

Glu Ile Gly Val Gln Phe Gln Ser Ala Ser Asp Ser Ser Gly Gln Thr
465 470 475 480

Ser Ile Tyr Ile Asp Asn Val Ile Val Glu
485 490

<210> 3
<211> 1438
<212> DNA
<213> Bacillus sp. I633

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tataaacaag caatcccgcg attgcgtaac gccggtctaa accatacctt gatggtagat 480
gctgcggggg ggggacaatt tccacaatcg attcatgatt atggaagaga agttttttaat 540

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 <211> 476
 <212> PRT
 <213> Bacillus

<400> 4

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Lys Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala
 35 40 45

Asn Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp
 50 55 60

Asp Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His
 65 70 75 80

212

E

Leu Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile
85 90 95

Ala Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala
100 105 110

Leu Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp
115 120 125

Phe Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala
130 135 140

Ile Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp
145 150 155 160

Ala Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg
165 170 175

Glu Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His
180 185 190

Met Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile
195 200 205

Asp Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly
210 215 220

His Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr
225 230 235 240

Ser Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn
245 250 255

Gly Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn
260 265 270

Asn Leu Thr Ala Trp Gly Asn Thr Ile Val Asn Gly Pro Tyr Gly Leu
275 280 285

Arg Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Ala Ser Pro Glu Pro
290 295 300

6 213

E

Thr Pro Glu Pro Thr Ala Asn Thr Pro Val Ser Gly Asn Leu Lys Val
305 310 315 320

Glu Phe Tyr Asn Ser Asn Pro Ser Asp Thr Thr Asn Ser Ile Asn Pro
325 330 335

Gln Phe Lys Val Thr Asn Thr Gly Ser Ser Ala Ile Asp Leu Ser Lys
340 345 350

Leu Thr Leu Arg Tyr Tyr Tyr Thr Val Asp Gly Gln Lys Asp Gln Thr
355 360 365

Phe Trp Cys Asp His Ala Ala Ile Ile Gly Ser Asn Gly Ser Tyr Asn
370 375 380

Gly Ile Thr Ser Asn Val Lys Gly Thr Phe Val Lys Met Ser Ser Ser
385 390 395 400

Thr Asn Asn Ala Asp Thr Tyr Leu Glu Ile Ser Phe Thr Gly Gly Thr
405 410 415

Leu Glu Pro Gly Ala His Val Gln Ile Gln Gly Arg Phe Ala Lys Asn
420 425 430

Asp Trp Ser Asn Tyr Thr Gln Ser Asn Asp Tyr Ser Phe Lys Ser Arg
435 440 445

Ser Gln Phe Val Glu Trp Asp Gln Val Thr Ala Tyr Leu Asn Gly Val
450 455 460

Leu Val Trp Gly Lys Glu Pro Gly Gly Ser Val Val
465 470 475

<210> 5
<211> 1482
<212> DNA
<213> Bacillus agaradhaerens

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aatacgttat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180
gcttggtata aagacaccgc ttcaacagct attcctgcca ttgcagagca aggcgccaac 240

214

E

acgattcgta ttgttttatc agatggcggt caatgggaaa aagacgacat tgacaccatt 300
 cgtgaagtca ttgagcttgc ggagcaaaat aaaatggtgg ctgtcgttga agttcatgat 360
 gccacgggtc gcgattcgcg cagtgattta aatcgagccg ttgattattg gatagaaatg 420
 aaagatgcgc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggat 480
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 gaaaatagtc atcatgttag ggaaataggc gtgcaatttt cagcggcaga taatagcagt 1440
 ggtcaaactg ctctatacgt tgataacgtt actttaagat ag 1482

<210> 6
 <211> 493
 <212> PRT
 <213> Bacillus

<400> 6

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Ile Ile Ser Val Gly Ile Met Gly Ile Thr Thr Ser Pro Ser Ala Ala
 20 25 30

8215

E

Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
35 40 45

Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
50 55 60

Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
65 70 75 80

Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
85 90 95

Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
100 105 110

Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
115 120 125

Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
130 135 140

Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
145 150 155 160

Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
165 170 175

Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
180 185 190

Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
195 200 205

Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
210 215 220

Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
225 230 235 240

Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
245 250 255

216

E

Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
260 265 270

Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
275 280 285

Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His
290 295 300

Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln
305 310 315 320

Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His
325 330 335

Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr
340 345 350

Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr
355 360 365

Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu
370 375 380

Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu
385 390 395 400

His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly
405 410 415

Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser
420 425 430

Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn
435 440 445

Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ser His
450 455 460

His Val Arg Glu Ile Gly Val Gln Phe Ser Ala Ala Asp Asn Ser Ser
465 470 475 480

Gly Gln Thr Ala Leu Tyr Val Asp Asn Val Thr Leu Arg
485 490

<210> 7
<211> 1407
<212> DNA
<213> *Bacillus agaradhaerens*

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<210> 8
<211> 468
<212> PRT
<213> Bacillus agaradhaerens

<400> 8

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Ile Ile Ser Val Gly Ile Met Gly Ile Thr Thr Ser Pro Ser Ala Ala
20 25 30

Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
35 40 45

Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
50 55 60

Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
65 70 75 80

Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
85 90 95

Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
100 105 110

Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
115 120 125

Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
130 135 140

Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
145 150 155 160

Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
165 170 175

Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
180 185 190

Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
195 200 205

Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
210 215 220

Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
225 230 235 240

Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
245 250 255

Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
260 265 270

Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
275 280 285

Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His
290 295 300

Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln
305 310 315 320

Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His
325 330 335

Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr
340 345 350

Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr
355 360 365

Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu
370 375 380

Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu
385 390 395 400

His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly
405 410 415

Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser

420

425

430

Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn
 435 440 445

Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ile Ile
 450 455 460

Met Leu Gly Lys
 465

<210> 9
 <211> 1761
 <212> DNA
 <213> Bacillus halodurans

<400> 9
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aaagtacaag atgaagtgat tagactttat gtaaaggctt cagaaatctc actttacaag 1560
cttacgtttg atgaggatat taatggaatt aagtcgaatg gcacttggcc tgaagatggt 1620
attacatctg acgttttctca tgtcagtttt gacggaaatg ggaaattgaa gtttgcagtt 1680
aatggaatgt catccgaaga gtggtggcaa gaacttaa atagaattaac agatctttct 1740
gatgtgaatt tagccaagta a 1761

<210> 10
<211> 586
<212> PRT
<213> Bacillus halodurans

<400> 10

Met Lys Ser Ile Lys Lys Leu Val Val Val Cys Met Ala Phe Leu Leu
1 5 10 15

Ile Phe Pro Ser Thr Ser Phe Ala Phe Ser Gly Ser Val Ser Ala Ser
20 25 30

Gly Gln Glu Leu Lys Met Thr Asp Gln Asn Ala Ser Gln Tyr Thr Lys
35 40 45

Glu Leu Phe Ala Phe Leu Arg Asp Val Ser Gly Lys Gln Val Leu Phe
50 55 60

Gly Gln Gln His Ala Thr Asp Glu Gly Leu Thr Leu Arg Gly Thr Gly
65 70 75 80

Asn Arg Ile Gly Ser Thr Glu Ser Glu Val Lys Asn Ala Val Gly Asp
85 90 95

Tyr Pro Ala Val Phe Gly Trp Asp Thr Asn Ser Leu Asp Gly Arg Glu

100

105

110

Lys Pro Gly Asn Asp Glu Pro Ser Gln Glu Gln Arg Ile Leu Asn Thr
115 120 125

Ala Ala Ser Met Lys Ala Ala His Asp Leu Gly Gly Ile Ile Thr Leu
130 135 140

Ser Met His Pro Asp Asn Phe Val Thr Gly Gly Ala Tyr Gly Asp Thr
145 150 155 160

Thr Gly Asn Val Val Gln Glu Ile Leu Pro Gly Gly Ser Lys His Glu
165 170 175

Glu Phe Asn Ala Trp Leu Asp Asn Leu Ala Ala Leu Ala His Glu Leu
180 185 190

Lys Asp Asp Asn Gly Lys His Ile Pro Ile Ile Phe Arg Pro Phe His
195 200 205

Glu Gln Thr Gly Ser Trp Phe Trp Trp Gly Ala Ser Thr Thr Thr Pro
210 215 220

Glu Gln Tyr Lys Ala Ile Tyr Arg Tyr Thr Val Glu Tyr Leu Arg Asp
225 230 235 240

Val Lys Gly Ala Asn Asn Phe Leu Tyr Gly Phe Ser Pro Gly Ala Gly
245 250 255

Pro Ala Gly Asp Leu Asn Arg Tyr Met Glu Thr Tyr Pro Gly Asp Asp
260 265 270

Tyr Val Asp Ile Phe Gly Ile Asp Asn Tyr Asp Asn Lys Ser Asn Ala
275 280 285

Gly Ser Glu Ala Trp Ile Gln Gly Val Val Thr Asp Leu Ala Met Leu
290 295 300

Val Asp Leu Ala Glu Glu Lys Gly Lys Ile Ala Ala Phe Thr Glu Tyr
305 310 315 320

Gly Tyr Ser Ala Thr Gly Met Asn Arg Thr Gly Asn Thr Leu Asp Trp
325 330 335

Tyr Thr Arg Leu Leu Asn Ala Ile Lys Glu Asp Pro Lys Ala Ser Lys
340 345 350

Ile Ser Tyr Met Leu Thr Trp Ala Asn Phe Gly Phe Pro Asn Asn Met
355 360 365

Tyr Val Pro Tyr Lys Asp Ile His Gly Asp Leu Gly Gly Asp His Glu
370 375 380

Leu Leu Pro Asp Phe Ile Lys Phe Phe Glu Asp Asp Tyr Ser Ala Phe
385 390 395 400

Thr Gly Asp Ile Lys Gly Asn Val Tyr Asp Thr Gly Ile Glu Tyr Thr
405 410 415

Val Ala Pro His Glu Arg Leu Met Tyr Val Leu Ser Pro Ile Thr Gly
420 425 430

Thr Thr Ile Thr Asp Thr Val Thr Leu Arg Ala Lys Val Leu Asn Asp
435 440 445

Asp Asn Ala Val Val Thr Tyr Arg Val Glu Gly Ser Asp Val Glu His
450 455 460

Glu Met Thr Leu Ala Asp Ser Gly Tyr Tyr Thr Ala Lys Tyr Ser Pro
465 470 475 480

Thr Ala Glu Val Asn Gly Gly Ser Val Asp Leu Thr Val Thr Tyr Trp
485 490 495

Ser Gly Glu Glu Lys Val Gln Asp Glu Val Ile Arg Leu Tyr Val Lys
500 505 510

Ala Ser Glu Ile Ser Leu Tyr Lys Leu Thr Phe Asp Glu Asp Ile Asn
515 520 525

Gly Ile Lys Ser Asn Gly Thr Trp Pro Glu Asp Gly Ile Thr Ser Asp
530 535 540

Val Ser His Val Ser Phe Asp Gly Asn Gly Lys Leu Lys Phe Ala Val
545 550 555 560

Asn Gly Met Ser Ser Glu Glu Trp Trp Gln Glu Leu Lys Leu Glu Leu
 565 570 575

Thr Asp Leu Ser Asp Val Asn Leu Ala Lys
 580 585

<210> 11
 <211> 995
 <212> DNA
 <213> Bacillus sp. AAI12

E
 <400> 11
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 ggtacaacat tatatgatgc aaatggaaac ccttttggtt tgagagggat taatcatgga 180
 catgcttggt ttaaacaaga actagaaaca tccatgagag ggattagtca aacaggggca 240
 aatacgattc gtgtcgtttt gtctaattggg caaagatggc aaaaagatga tcgaaacatg 300
 gtagcttcgg ttatttcttt ggcagagcag catcaaatga ttgccgtttt agaagttcat 360
 gatgctactg gtagcaataa tttctccgat ctgcaagctg ctgtggacta ttggattgag 420
 atgaaggatg ttttgcaggg gaaagaggac atagtgatca ttaatatcgc caatgaatgg 480
 tacggtgctt gggacggagg cgcattgggca cgaggggtatc agaatgcgat acgtcagctt 540
 cgaaatgcag gcttgtcaca tacatttatg gttgacgctg ccggttatgg ccagtaccct 600
 caatcggtag ttgattatgg tcaagaagta ttaaatgctg acccacagag aaacacaatt 660
 ttttctgttc atatgtatga atatgcaggc ggagatgcta atacagtaag acgaaacatt 720
 gactcgatct taagccagaa cttagctctt gtcattgggtg aattcgggca ttggcattat 780
 gacggtgatg ttgatgagga caccatttta agctattcac agcaaagaaa tgtgggatgg 840
 ttggcgtgga gctggcatgg caatagtga ggggtcgaat atcttgattt atcgaatgac 900
 tttgctggta atcgactgac atgggtgggt gatcgaatag taaacgggtcc gaatgggatt 960
 cgtcaaacct ctaaaagaag cagtgtgttt caata 995

<210> 12
 <211> 331
 <212> PRT
 <213> Bacillus sp. AAI12

<400> 12

Val Tyr Lys Leu Thr His Thr Tyr Phe Val Ala Leu Ile Cys Ser Ile
1 5 10 15

Leu Ile Phe Ala Gly Val Leu Asn Thr Ser Ser Ser Gln Ala Glu Ala
20 25 30

His His Ser Gly Phe His Val Asn Gly Thr Thr Leu Tyr Asp Ala Asn
35 40 45

Gly Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Phe
50 55 60

Lys Gln Glu Leu Glu Thr Ser Met Arg Gly Ile Ser Gln Thr Gly Ala
65 70 75 80

Asn Thr Ile Arg Val Val Leu Ser Asn Gly Gln Arg Trp Gln Lys Asp
85 90 95

Asp Arg Asn Met Val Ala Ser Val Ile Ser Leu Ala Glu Gln His Gln
100 105 110

Met Ile Ala Val Leu Glu Val His Asp Ala Thr Gly Ser Asn Asn Phe
115 120 125

Ser Asp Leu Gln Ala Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Val
130 135 140

Leu Gln Gly Lys Glu Asp Ile Val Ile Ile Asn Ile Ala Asn Glu Trp
145 150 155 160

Tyr Gly Ala Trp Asp Gly Gly Ala Trp Ala Arg Gly Tyr Gln Asn Ala
165 170 175

Ile Arg Gln Leu Arg Asn Ala Gly Leu Ser His Thr Phe Met Val Asp
180 185 190

Ala Ala Gly Tyr Gly Gln Tyr Pro Gln Ser Val Val Asp Tyr Gly Gln
195 200 205

Glu Val Leu Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Val His
210 215 220

Met Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Arg Asn Ile

225

230

235

240

Asp Ser Ile Leu Ser Gln Asn Leu Ala Leu Val Ile Gly Glu Phe Gly
245 250 255

His Trp His Tyr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr
260 265 270

Ser Gln Gln Arg Asn Val Gly Trp Leu Ala Trp Ser Trp His Gly Asn
275 280 285

Ser Glu Gly Val Glu Tyr Leu Asp Leu Ser Asn Asp Phe Ala Gly Asn
290 295 300

Arg Leu Thr Trp Trp Gly Asp Arg Ile Val Asn Gly Pro Asn Gly Ile
305 310 315 320

Arg Gln Thr Ser Lys Arg Ser Ser Val Phe Gln
325 330

<210> 13

<211> 1464

<212> DNA

<213> Humicola insolens

<400> 13

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gccgctcctt actgtgctcc ccagccgtcg acaacctctc aggagcctac gagcactccg 120
tcgcctgtgc ccgggtccgcg gaccttcgaa gcggaggatg ccatcctcac gggcacgagg 180
gttgagtcga gcctcgccgg ctactctggt accggatatg tagcgggctt cgacgagccc 240
agtgacaaga tcacgttcca cgtggacagc gagaccacac ggctgtacga cctcaccatc 300
cgcggtggccg ccatctatgg cgagaagcgc accaccgtcg tgctcaataa cggcgcgga 360
agtgagggtct acttcccggc aggcgattcg ttcgtcgaca tcgctgccgg ccaggtcctg 420
ctgaaccagg gcgacaacac catcgacatt gtcaacaact ggggatggta cctgatcgac 480
tccatcacca tcaccccctc cgccccgcga cccctcacc aaatcaaccc tcccccgtc 540
aaccctgccg ccgacgacaa cgcgcgggcg ttgtacgcat acctccgctc catctacggc 600
aagaaaatcc tttccggcca gcaggagctt tcctgggcca actggatcgc ccaacagacg 660
ggcaaaaactc ccgcgctggt gtccgtcgat atgatggatt attcccctag tcgggtggaa 720

agaggcactg tcgggtctgc cgtcaggag gccatcgagc atcaccggcg cggcggcatt 780
 gtctcggtgt tgtggcactg gaacgcgccc acggggctgt acgacacgcc cgagcgccgg 840
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 gggttggtttt ggtggggagc gaagggcccg gaggcataca agaagctgtg ggggattctg 1080
 tatgaccgac tcacgaacta ccatgggctg aataacctgc tgtgggtgtg gaactcgatc 1140
 ctacccgagt ggtatcccgg agacgaaaca gtagacattg tcagcgcgga cgtgtacgcg 1200
 cagggtaatg ggcccattgc gacgcagtat aaccagctca tcgagctggg caaggacaag 1260
 aagatgatcg cggcgactga ggtcggggcc gcgccgctgc cggacctgtt gcaggcctat 1320
 gaggctcact gggtgtggtt cgctgtttgg ggagacacgt tcatcaacaa ccctcagtgg 1380
 aactcgatcg agaccttgaa gacgatctac aatagcgact atgttctcac tctcgatgag 1440
 attcaggggt ggaggaacgc gcaa 1464

<210> 14
 <211> 488
 <212> PRT
 <213> Humicola insolens

<400> 14

Met Ala Lys Ala Leu Lys Tyr Phe Ala Trp Gly Leu Ala Ala Leu Ala
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Ser Gly Ala Val Ala Ala Pro Tyr Cys Ala Pro Gln Pro Ser Thr Thr
 20 25 30

Ser Gln Glu Pro Thr Ser Thr Pro Ser Pro Val Pro Gly Pro Arg Thr
 35 40 45

Phe Glu Ala Glu Asp Ala Ile Leu Thr Gly Thr Arg Val Glu Ser Ser
 50 55 60

Leu Ala Gly Tyr Ser Gly Thr Gly Tyr Val Ala Gly Phe Asp Glu Pro
 65 70 75 80

Ser Asp Lys Ile Thr Phe His Val Asp Ser Glu Thr Thr Arg Leu Tyr
 85 90 95

Asp Leu Thr Ile Arg Val Ala Ala Ile Tyr Gly Glu Lys Arg Thr Thr
100 105 110

Val Val Leu Asn Asn Gly Ala Ala Ser Glu Val Tyr Phe Pro Ala Gly
115 120 125

Asp Ser Phe Val Asp Ile Ala Ala Gly Gln Val Leu Leu Asn Gln Gly
130 135 140

E Asp Asn Thr Ile Asp Ile Val Asn Asn Trp Gly Trp Tyr Leu Ile Asp
145 150 155 160

Ser Ile Thr Ile Thr Pro Ser Ala Pro Arg Pro Pro His Gln Ile Asn
165 170 175

Pro Ser Pro Val Asn Pro Ala Ala Asp Asp Asn Ala Arg Ala Leu Tyr
180 185 190

Ala Tyr Leu Arg Ser Ile Tyr Gly Lys Lys Ile Leu Ser Gly Gln Gln
195 200 205

Glu Leu Ser Trp Ala Asn Trp Ile Ala Gln Gln Thr Gly Lys Thr Pro
210 215 220

Ala Leu Val Ser Val Asp Met Met Asp Tyr Ser Pro Ser Arg Val Glu
225 230 235 240

Arg Gly Thr Val Gly Ser Ala Val Glu Glu Ala Ile Glu His His Arg
245 250 255

Arg Gly Gly Ile Val Ser Val Leu Trp His Trp Asn Ala Pro Thr Gly
260 265 270

Leu Tyr Asp Thr Pro Glu Arg Arg Trp Trp Ser Gly Phe Tyr Thr Asp
275 280 285

Ala Thr Asp Phe Asp Val Ala Arg Ala Leu Ala Asp Thr Thr Asn Ala
290 295 300

Asn Tyr Thr Leu Leu Ile Arg Asp Ile Asp Ala Ile Ala Val Gln Leu
305 310 315 320

Lys Arg Leu Arg Asp Ala Gly Val Pro Val Leu Trp Arg Pro Leu His
 325 330 335

Glu Ala Glu Gly Gly Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Ala
 340 345 350

Tyr Lys Lys Leu Trp Gly Ile Leu Tyr Asp Arg Leu Thr Asn Tyr His
 355 360 365

Gly Leu Asn Asn Leu Leu Trp Val Trp Asn Ser Ile Leu Pro Glu Trp
 370 375 380

Tyr Pro Gly Asp Glu Thr Val Asp Ile Val Ser Ala Asp Val Tyr Ala
 385 390 395 400

Gln Gly Asn Gly Pro Met Ser Thr Gln Tyr Asn Gln Leu Ile Glu Leu
 405 410 415

Gly Lys Asp Lys Lys Met Ile Ala Ala Thr Glu Val Gly Ala Ala Pro
 420 425 430

Leu Pro Asp Leu Leu Gln Ala Tyr Glu Ala His Trp Leu Trp Phe Ala
 435 440 445

Val Trp Gly Asp Thr Phe Ile Asn Asn Pro Gln Trp Asn Ser Ile Glu
 450 455 460

Thr Leu Lys Thr Ile Tyr Asn Ser Asp Tyr Val Leu Thr Leu Asp Glu
 465 470 475 480

Ile Gln Gly Trp Arg Asn Ala Gln
 485

<210> 15
 <211> 1107
 <212> DNA
 <213> Bacillus sp. AA349

<400> 15
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 aacttagtag ttgcgcaagc tagtggacat gggcaaagtc ataaagtacc ttgggcacca 120
 caagctgaag cacctggaaa aacggctgaa aatggagtct gggataaagt tcgaaataat 180
 cctggaaaag ccaatcctcc agcaggaaaa gtcaatgggt tttatataga tggaacaacc 240

230

E

ttatatgatg caaatggtaa gccatttgtg atgctgggaa ttaaccacgg tcattcatgg 300
 tacaagcctc acatagaaac cgcgatggag gcaattgctg atactggagc aaactccatt 360
 cgtgtagtgc tctcagatgg acaacagtgg accaaagatg atgttgacga agtagcaaaa 420
 attatatctt tagcagaaaa acattcttta gttgctgctc ttgaggtaca tgatgcactc 480
 ggaacagatg atattgaacc attacttaaa acagttgatt actggattga gatcaaagat 540
 gctttaatcg gaaaagagga caaagtaatt attaacattt ctaatgaatg gtttggttct 600
 tggagcagtg aagggtgggc agatggatat aaaaaagcaa ttcctttact aagagaggcg 660
 ggtctaaaac atacacttat ggttgacgca gctgggtggg gacaatttcc tagatctatt 720
 catgaaaaag gattagaagt ttttaactca gaccatttaa agaatacaat gttttccatt 780
 catatgtatg aatgggcagc gggtaatcct caacaagtaa aagacaatat tgacgggtgtt 840
 cttgaaaaga atttagctgt agtaattggg gagttcggtc atcatcacta cggaagagat 900
 gttgctgttg atacaatctt aagtcattct gagaagtatg atgtagggtg gcttgcttgg 960
 tcttggcacg gaaatagtgg tgggtgtagag tatcttgact tagcaacaga tttctcaggg 1020
 acacaactaa ctgaatgggg agaaagaatt gtacacgggc cgaatgggtt aaaagaaaact 1080
 tctgaaatcg ttagtgtata caaaaaa 1107

<210> 16
 <211> 369
 <212> PRT
 <213> Bacillus sp.

<400> 16

Met Arg Ser Met Lys Leu Leu Phe Ala Met Phe Ile Leu Val Phe Ser
 1 5 10 15

Ser Phe Thr Phe Asn Leu Val Val Ala Gln Ala Ser Gly His Gly Gln
 20 25 30

Met His Lys Val Pro Trp Ala Pro Gln Ala Glu Ala Pro Gly Lys Thr
 35 40 45

Ala Glu Asn Gly Val Trp Asp Lys Val Arg Asn Asn Pro Gly Lys Ala
 50 55 60

Asn Pro Pro Ala Gly Lys Val Asn Gly Phe Tyr Ile Asp Gly Thr Thr
 65 70 75 80

Leu Tyr Asp Ala Asn Gly Lys Pro Phe Val Met Arg Gly Ile Asn His
85 90 95

Gly His Ser Trp Tyr Lys Pro His Ile Glu Thr Ala Met Glu Ala Ile
100 105 110

Ala Asp Thr Gly Ala Asn Ser Ile Arg Val Val Leu Ser Asp Gly Gln
115 120 125

Gln Trp Thr Lys Asp Asp Val Asp Glu Val Ala Lys Ile Ile Ser Leu
130 135 140

Ala Glu Lys His Ser Leu Val Ala Ala Leu Glu Val His Asp Ala Leu
145 150 155 160

Gly Thr Asp Asp Ile Glu Pro Leu Leu Lys Thr Val Asp Tyr Trp Ile
165 170 175

Glu Ile Lys Asp Ala Leu Ile Gly Lys Glu Asp Lys Val Ile Ile Asn
180 185 190

Ile Ser Asn Glu Trp Phe Gly Ser Trp Ser Ser Glu Gly Trp Ala Asp
195 200 205

Gly Tyr Lys Lys Ala Ile Pro Leu Leu Arg Glu Ala Gly Leu Lys His
210 215 220

Thr Leu Met Val Asp Ala Ala Gly Trp Gly Gln Phe Pro Arg Ser Ile
225 230 235 240

His Glu Lys Gly Leu Glu Val Phe Asn Ser Asp Pro Leu Lys Asn Thr
245 250 255

Met Phe Ser Ile His Met Tyr Glu Trp Ala Ala Gly Asn Pro Gln Gln
260 265 270

Val Lys Asp Asn Ile Asp Gly Val Leu Glu Lys Asn Leu Ala Val Val
275 280 285

Ile Gly Glu Phe Gly His His His Tyr Gly Arg Asp Val Ala Val Asp
290 295 300

Thr Ile Leu Ser His Ser Glu Lys Tyr Asp Val Gly Trp Leu Ala Trp
305 310 315 320

Ser Trp His Gly Asn Ser Gly Gly Val Glu Tyr Leu Asp Leu Ala Thr
325 330 335

Asp Phe Ser Gly Thr Gln Leu Thr Glu Trp Gly Glu Arg Ile Val His
340 345 350

Gly Pro Asn Gly Leu Lys Glu Thr Ser Glu Ile Val Ser Val Tyr Lys
355 360 365

Lys

<210> 17
<211> 915
<212> DNA
<213> Bacillus sp.

<400> 17
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ggacaaaatt catcgccaat taaagcttat ggcaacgaag tgtaaacca tgatccgcag 120
cgcaatgtta tggttctccat acacatgtac ggttcctgga ataatcagtc gcgaatcggc 180
agcgaattgc aggccatcaa agaccttggc cttgctgtca tgattgggtga attcgggatac 240
aactacaaca acggcaataa caacttgggg agtcagggtta acgcccagga aatcatgaat 300
caggcgcaag caaaaaggaat cggctacatg ccgtggctcg ggactggcaa tgacgcggct 360
aactcttggc ttgatattgac aacaaacgat tggcaaacac ttacatcatg ggggaatcta 420
gttgtaaatg gaaccaacgc cattcgagct acgtctgtcc cagcaactgt atttaataca 480
caaacaacaa tttatgattt tgaaggcggc aatgcccagg gctggtcagg ttccgggttg 540
agcggggggc cttgggtctgt taatgaatgg gcggcgagcg gtagttattc tctcaaagcg 600
aatatatctc taggcgccac tcaaaaagct ttgcaaacca cagcgtccca taatttcagc 660
ggccggtcta cattatccgt aagagtaaag catgcagcat ggggaaatca cggcagcggc 720
atgcaagcca agttatatgt gaaaacaggg gccggttacg cctgggtatga tggcggcact 780
gtaaacatca acagctcggg caacacattg acgctaaacc tggcaggcat tcctaattctg 840
aacgacgtca gagaactcgg aattgaattt ataacacctg caaattcgag tggttctttc 900

gcaatttatg ttgac

915

<210> 18
<211> 305
<212> PRT
<213> Bacillus sp.

<400> 18

Ile Ser Thr Leu Arg Asn Ala Gly Ile Arg Asn Thr Ile Val Val Asp
1 5 10 15

Ala Ser Gly Trp Gly Gln Asn Ser Ser Pro Ile Lys Ala Tyr Gly Asn
20 25 30

Glu Val Leu Asn His Asp Pro Gln Arg Asn Val Met Phe Ser Ile His
35 40 45

Met Tyr Gly Ser Trp Asn Asn Gln Ser Arg Ile Gly Ser Glu Leu Gln
50 55 60

Ala Ile Lys Asp Leu Gly Leu Ala Val Met Ile Gly Glu Phe Gly Tyr
65 70 75 80

Asn Tyr Asn Asn Gly Asn Asn Asn Leu Gly Ser Gln Val Asn Ala Gln
85 90 95

Glu Ile Met Asn Gln Ala Gln Ala Lys Gly Ile Gly Tyr Met Pro Trp
100 105 110

Ser Trp Thr Gly Asn Asp Ala Ala Asn Ser Trp Leu Asp Met Thr Thr
115 120 125

Asn Asp Trp Gln Thr Leu Thr Ser Trp Gly Asn Leu Val Val Asn Gly
130 135 140

Thr Asn Gly Ile Arg Ala Thr Ser Val Pro Ala Thr Val Phe Asn Thr
145 150 155 160

Gln Thr Thr Ile Tyr Asp Phe Glu Gly Gly Asn Ala Gln Gly Trp Ser
165 170 175

Gly Ser Gly Leu Ser Gly Gly Pro Trp Ser Val Asn Glu Trp Ala Ala
180 185 190

Ser Gly Ser Tyr Ser Leu Lys Ala Asn Ile Ser Leu Gly Ala Thr Gln
 195 200 205

Lys Ala Leu Gln Thr Thr Ala Ser His Asn Phe Ser Gly Arg Ser Thr
 210 215 220

Leu Ser Val Arg Val Lys His Ala Ala Trp Gly Asn His Gly Ser Gly
 225 230 235 240

Met Gln Ala Lys Leu Tyr Val Lys Thr Gly Ala Gly Tyr Ala Trp Tyr
 245 250 255

Asp Gly Gly Thr Val Asn Ile Asn Ser Ser Gly Asn Thr Leu Thr Leu
 260 265 270

Asn Leu Ala Gly Ile Pro Asn Leu Asn Asp Val Arg Glu Leu Gly Ile
 275 280 285

Glu Phe Ile Thr Pro Ala Asn Ser Ser Gly Ser Phe Ala Ile Tyr Val
 290 295 300

Asp
 305

<210> 19
 <211> 397
 <212> DNA
 <213> Bacillus clausii

<400> 19
 atctctcagg gcttggtagg agtcattatt ctcttataca tggcatttag tcaagagaga 60
 ggattggcgc aaactggatt tcaagtaaca gggacccagt tgcttgatgg agagggcaat 120
 ccgtatgtga tgcgtggagt caatcacgga cattcatggt tcaaacaaga ccttgataca 180
 gcaataccag ctattgcagc gactggcgct aatacgggta gaatcgtttt atcgaatggc 240
 caacaatggg agcgagatac cgtagcggaa gttgaaagag tgcttgcagt taccgaagag 300
 gaaggcttga cggctgtact tgaagttcat gatgcgacgg gaagtgatga tccaaacgat 360
 ttgtttactg cagtggagta ttggtcagag agaggat 397

<210> 20
 <211> 132
 <212> PRT

<213> Bacillus clausii

<400> 20

Ile Ser Gln Gly Leu Val Gly Val Ile Ile Leu Leu Tyr Met Ala Phe
1 5 10 15

Ser Gln Glu Arg Gly Leu Ala Gln Thr Gly Phe Gln Val Thr Gly Thr
20 25 30

Gln Leu Leu Asp Gly Glu Gly Asn Pro Tyr Val Met Arg Gly Val Asn
35 40 45

His Gly His Ser Trp Phe Lys Gln Asp Leu Asp Thr Ala Ile Pro Ala
50 55 60

Ile Ala Ala Thr Gly Ala Asn Thr Val Arg Ile Val Leu Ser Asn Gly
65 70 75 80

Gln Gln Trp Glu Arg Asp Thr Val Ala Glu Val Glu Arg Val Leu Ala
85 90 95

Val Thr Glu Glu Glu Gly Leu Thr Ala Val Leu Glu Val His Asp Ala
100 105 110

Thr Gly Ser Asp Asp Pro Asn Asp Leu Phe Thr Ala Val Glu Tyr Trp
115 120 125

Ser Glu Arg Gly
130

<210> 21

<211> 960

<212> DNA

<213> Bacillus sp.

<400> 21

atgaatcgta agcgggttaca atggggttga gcactagtgg tgggtgttggt tttgtttgta 60
tacagtagcg gtttagcatc tgcacaaagc ggctttcacg taaaagggtac agagttgttg 120
gacaaaaatg gcgatcctta cgttatgcgt ggcgtcaacc atggacattc ttggtttaaa 180
caagatttag aggaggcaat ccctgccata gcagaaacag gggcgaacac agtgagaatc 240
gtcttatcca atggacagca atgggaaaaa gatgatgcct ctgagcttgc ccgtgtgctt 300
gtgcccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360

gataatcccg atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420
aaggggacag aagaccgggt aatcattaac attgccaatg aatgggatgg ggcgtggagg 480
agtgacgttt gggcagaggc atacgcacaa gcgatcccg gcttgcgag tgctggcctc 540
gcccatacgt taatagttga tgcggcaggt tggggacagt accctgcctc tatccatgag 600
cggggagccg acgtatttgc ctccgatcca ttaaaaaaca caatgttttc catccatag 660
tacgaatatg caggagcgga tagggcgaca gtttctgaaa acatcgacgg tgtacttgct 720
gaaaatcttg ctgtggtaat cgggtgaattt ggccataggc atcatgatgg cgatgtcgat 780
gaagatgcga ttttggccta tacagcagag cggcaagtgg gctggcttgc ctggatcatg 840
tatggcaata gcgggggtgt tgaatacttg gatttaactg aaggcccatc aggtccatta 900
acgagttggg gcgaacggat tgtctatggg gaaatgggct taaaagtaat tgatcacttg 960

<210> 22
<211> 320
<212> PRT
<213> Bacillus sp.

<400> 22

Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Val Val Leu
1 5 10 15

Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe
20 25 30

His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val
35 40 45

Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu
50 55 60

Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile
65 70 75 80

Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu
85 90 95

Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu
100 105 110

Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys
115 120 125

Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu
130 135 140

Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg
145 150 155 160

Ser Asp Val Trp Ala Glu Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg
165 170 175

Ser Ala Gly Leu Ala His Thr Leu Ile Val Asp Ala Ala Gly Trp Gly
180 185 190

Gln Tyr Pro Ala Ser Ile His Glu Arg Gly Ala Asp Val Phe Ala Ser
195 200 205

Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met Tyr Glu Tyr Ala
210 215 220

Gly Ala Asp Arg Ala Thr Val Ser Glu Asn Ile Asp Gly Val Leu Ala
225 230 235 240

Glu Asn Leu Ala Val Val Ile Gly Glu Phe Gly His Arg His His Asp
245 250 255

Gly Asp Val Asp Glu Asp Ala Ile Leu Ala Tyr Thr Ala Glu Arg Gln
260 265 270

Val Gly Trp Leu Ala Trp Ser Trp Tyr Gly Asn Ser Gly Gly Val Glu
275 280 285

Tyr Leu Asp Leu Thr Glu Gly Pro Ser Gly Pro Leu Thr Ser Trp Gly
290 295 300

Glu Arg Ile Val Tyr Gly Glu Met Gly Leu Lys Val Ile Asp His Leu
305 310 315 320

<210> 23
<211> 564
<212> DNA
<213> Bacillus sp.

<400> 23
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gctgccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360
gataatcccg atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420
aaggggacag aagaccgggt aatcattaac attgccaatg aatgggtatgg ggcgtggagg 480
agtgcctttt gggcaaaaagc atacgcacaa gcgatcccg ccttgccgag tgctggcctc 540
gcccatacgt taataattga tgcc 564

<210> 24
<211> 188
<212> PRT
<213> Bacillus sp.

<400> 24

Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Ala Val Leu
1 5 10 15

Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe
20 25 30

His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val
35 40 45

Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu
50 55 60

Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile
65 70 75 80

Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu
85 90 95

Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu
100 105 110

Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys
 115 120 125

Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu
 130 135 140

Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg
 145 150 155 160

Ser Asp Leu Trp Ala Lys Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg
 165 170 175

Ser Ala Gly Leu Ala His Thr Leu Ile Ile Asp Ala
 180 185

<210> 25
 <211> 2445
 <212> DNA
 <213> Bacillus sp.

<400> 25
 atgaacaaac aaccgttaaa gactgcattt attatgttgt tatgtagcgt gtttatgttt 60
 caaagcctac cttactatgt gaacgctatc aatgaaggcg agagagaagc ttttgcaccc 120
 gcagggagat atgatgctga acaggcgact acgacaggaa atgccgtatt cacgaccgag 180
 cctgttgagg acggcgagta cgccggtccg ggctacattt ctttcttttc tgaagattcc 240
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 ttatctatcg gatactatgc tccatacggg aacaagggaa ccacaattct ggtgaacggg 360
 gcaggtaacg gagagtttat gttgccagcg cccgaggacg gggcagtcct cgccgaagtg 420
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 gggtattacg gcattgaata tattcgggtc gagccgggta atccaacgtt accgactata 540
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 gaaggttatt ccggagcagg ctatttggtc aaccaagagg ggacaattca ttggaatgta 660
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 cttgagccga cagttacgaa gctcattatt cttctgcac tagccggcac attagacgga 2340
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 gacgagcagc aatccggcag cgcgtatgag ttagtgctgg agatc 2445

<210> 26
 <211> 815
 <212> PRT
 <213> Bacillus sp.

<400> 26

Met Asn Lys Gln Pro Leu Lys Thr Ala Phe Ile Met Leu Leu Cys Ser
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Val Phe Met Phe Gln Ser Leu Pro Tyr Tyr Val Asn Ala Ile Asn Glu
20 25 30

Gly Glu Arg Glu Ala Phe Ala Ser Ala Gly Arg Tyr Asp Ala Glu Gln
35 40 45

Ala Thr Thr Thr Gly Asn Ala Val Phe Thr Thr Glu Pro Val Glu Asp
50 55 60

Gly Glu Tyr Ala Gly Pro Gly Tyr Ile Ser Phe Phe Ser Glu Asp Ser
65 70 75 80

Ser Pro Pro Ser Ser Ser Thr Thr Phe His Ile Gln Ala Asp Lys Thr
85 90 95

Glu Leu Tyr His Leu Ser Ile Gly Tyr Tyr Ala Pro Tyr Gly Asn Lys
100 105 110

Gly Thr Thr Ile Leu Val Asn Gly Ala Gly Asn Gly Glu Phe Met Leu
115 120 125

Pro Ala Pro Glu Asp Gly Ala Val Ser Ala Glu Val Glu Ile Ser Lys
130 135 140

Ile Leu Leu Glu Glu Gly Asn Asn Thr Ile Thr Phe Thr Arg Gly Trp
145 150 155 160

Gly Tyr Tyr Gly Ile Glu Tyr Ile Arg Val Glu Pro Val Asn Pro Thr
165 170 175

Leu Pro Thr Ile Phe Ile Glu Ala Glu Glu Asp Tyr Glu Ala Thr Gly
180 185 190

Asn Val Ser Val Thr Asn Glu Ile Glu Gly Tyr Ser Gly Ala Gly Tyr
195 200 205

Leu Phe Asn Gln Glu Gly Thr Ile His Trp Asn Val Thr Ser Pro Glu
210 215 220

Thr Ser Ile Tyr Glu Val Ile Val Ala Tyr Ala Ala Pro Tyr Gly Asp
225 230 235 240

Lys Gln Thr Asn Leu Thr Val Asn Gly Gln Gly Thr Val Asn Leu Asp
245 250 255

Leu Lys Glu Thr Glu Val Phe Val Glu Leu Asn Val Gly Ile Val Ser
260 265 270

Leu Asn Glu Gly Glu Asn Thr Leu Thr Leu His Ser Gly Trp Gly Trp
275 280 285

Tyr Asn Ile Asp Tyr Ile Lys Leu Val Pro Val Val Ser Ser Asp Pro
290 295 300

Glu Pro His Gln Val Glu Lys Thr Leu Val Asn Pro Asp Ala Ser Pro
305 310 315 320

Glu Ala Arg Ala Leu Ile Asn Tyr Leu Val Asp Gln Tyr Gly Asn Lys
325 330 335

Ile Leu Ser Gly Gln Thr Glu Leu Lys Asp Ala Arg Trp Ile His Glu
340 345 350

Gln Val Gly Lys Tyr Pro Ala Val Met Ala Val Asp Phe Met Asp Tyr
355 360 365

Ser Pro Ser Arg Val Val His Gly Ala Thr Gly Thr Ala Val Glu Glu
370 375 380

Ala Ile Glu Trp Ala Glu Met Gly Gly Ile Ile Thr Phe His Trp His
385 390 395 400

Trp Asn Ala Pro Lys Asp Leu Leu Asn Val Pro Gly Asn Glu Trp Trp
405 410 415

Ser Gly Phe Tyr Thr Arg Ala Thr Thr Phe Asp Val Glu Tyr Ala Leu
420 425 430

Glu Asn Arg Glu Ser Glu Asp Phe Gln Leu Leu Ile Ser Asp Met Asp
435 440 445

Val Ile Ala Glu Gln Leu Lys Arg Leu Gln Ala Glu Asn Ile Pro Val
450 455 460

Leu Trp Arg Pro Leu His Glu Ala Glu Gly Gly Trp Phe Trp Trp Gly
465 470 475 480

Ala Lys Gly Pro Glu Ala Ala Ile Glu Leu Tyr Arg Leu Met Tyr Asp
485 490 495

Arg Tyr Thr Asn His His Lys Leu Asn Asn Leu Ile Trp Met Trp Asn
500 505 510

Ser Glu Ala Glu Glu Trp Tyr Pro Gly Asp Asp Val Val Asp Met Ile
515 520 525

Ser Thr Asp Ile Tyr Asn Pro Val Gly Asp Phe Ser Pro Ser Ile Asn
530 535 540

Lys Tyr Glu His Leu Lys Glu Leu Val Gln Asp Lys Lys Leu Val Ala
545 550 555 560

Leu Pro Glu Thr Gly Ile Ile Pro Asp Pro Asp Gln Leu Gln Leu Phe
565 570 575

Asn Ala Asn Trp Ser Trp Phe Ala Thr Trp Thr Gly Asp Tyr Ile Arg
580 585 590

Asp Gly Ile Ser Asn Pro Ile Glu His Leu Gln Lys Val Phe His His
595 600 605

Asp Tyr Val Ile Thr Leu Asp Glu Leu Pro Glu Asn Leu Ser Arg Tyr
610 615 620

Gly Leu Ser Glu Gly Val Trp Lys Ser Asp Ala Asp Leu Ser Val Lys
625 630 635 640

Thr Arg Thr Thr Ser Glu Ile Thr Val Asn Trp Ser Asn Ala Ile Gln
645 650 655

Tyr Asp Ser Val Asn Gly Tyr Lys Leu Ile Lys Asp Gly Val Glu Thr
660 665 670

Val Ser Val Glu Gly Gly Val Gln Glu Tyr Thr Phe Thr Asn Leu Leu

675

680

685

Pro Gly Thr Gln Tyr Thr Ile Lys Val Glu Ala Leu Asp Gln Asp Asp
690 695 700

Arg Trp Thr Ala Asp Gly Pro Val Ala Val Val Ser Thr Leu Ser Asn
705 710 715 720

Ala Pro Ile Ser Tyr Pro Pro Ala Val Thr Pro Asp Glu Pro Asn Glu
725 730 735

Glu Leu Ser Glu Gly Glu Tyr Thr Leu Leu Ala Asp Asp Leu Ser Ser
740 745 750

Gln Asp Gly Val Leu Glu Val Ser Leu Glu Pro Thr Val Thr Lys Leu
755 760 765

Ile Ile Pro Ser Ala Leu Ala Gly Thr Leu Asp Gly Asp Leu Arg Ile
770 775 780

Gly Tyr Gly Asp Val Trp Ile Val Ile Pro His Glu Gln Leu Gly Gly
785 790 795 800

Asp Glu Gln Gln Ser Gly Ser Ala Tyr Glu Leu Val Leu Glu Ile
805 810 815

<210> 27

<211> 1488

<212> DNA

<213> Bacillus sp.

<400> 27

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gtaagaatat ttgaagctga agatgctatt ttaaattgggc tgactattaa aaattctgaa 180
ccagggttttt ctggtaccgg atatgtaggt gactttgaaa atagctctca gagtgtgacg 240
tttcaaattg aggctcctaa agccggttta tacaacttaa atattggata tggcgcgatt 300
tatggaagtg gaaaagtagc taatgttatt gtaaattggag agaagctaag tactttttaca 360
atgggaagtg gcttttgtaa agcgtcagca ggaaaggat tacttaattc aggcttaaat 420
actatctcga ttactcctaa ttggacatgg tttaccattg attatattga agttatacat 480

gcaccggaac cggaaaacca taatgtagaa aagacgttaa ttaacccaaa tgcaacggat 540
gaagccaaag ctttaataag ctatctagtt gataactttg gtgagaaaat tcttgagg 600
caacatgatt atccaaatac acgaccacga gatttagaat atatttatga aactactggg 660
aagtatcctg ctgttttagg tttagacttt attgataaca gtccttctag agttgagcgc 720
ggagcctctg ctgatgaaac accagtagct attgactggg ggaataaagg gggaattgtt 780
actttcacct ggcattggaa tgctcccaa gatttattag atgaaccagg aaatgaatgg 840
tgagtggtt tttatacgag agcaacaact tttgacgtag aatatgcttt aaaacatccg 900
aagtcggagg actacatgct tctaatacgt gatattgatg taatagctgg tgaactaaag 960
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gatagaatga cgaactacca taacttaaat aatttaatat gggatatgaa ttccattgaa 1140
gaggattggt atcctggaga tgagtatgtc gatattgtaa gcttcgattc atatccagg 1200
gaatataact atagtccaat gagccgtgag tatgaagcac ttaaagagtt gtctagtaac 1260
aagaaactta tagcaatagc agaaaatgga ccaataccag atcctgattt actacaactt 1320
taccatgcta actatagttg gtttgctaca tggaatggag atatattaag aaatcaaaat 1380
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cctaacctta aaacatatag gggaagatgc acttatacag acactatc 1488

<210> 28
<211> 496
<212> PRT
<213> Bacillus sp.

<400> 28

Met Arg Asn Glu Lys Ile Arg Pro Phe Thr Lys Ile Lys Ala Ser Val
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Val Thr Ser Val Leu Leu Leu Thr Ile Ser Leu Ile Phe Thr Ile Gly
20 25 30

Asn Ile Ala Asn Ala Glu Ser Glu Val Arg Ile Phe Glu Ala Glu Asp
35 40 45

Ala Ile Leu Asn Gly Leu Thr Ile Lys Asn Ser Glu Pro Gly Phe Ser
50 55 60

Gly Thr Gly Tyr Val Gly Asp Phe Glu Asn Ser Ser Gln Ser Val Thr
65 70 75 80

Phe Gln Ile Glu Ala Pro Lys Ala Gly Leu Tyr Asn Leu Asn Ile Gly
85 90 95

Tyr Gly Ala Ile Tyr Gly Ser Gly Lys Val Ala Asn Val Ile Val Asn
100 105 110

Gly Glu Lys Leu Ser Thr Phe Thr Met Gly Ser Gly Phe Gly Lys Ala
115 120 125

Ser Ala Gly Lys Val Leu Leu Asn Ser Gly Leu Asn Thr Ile Ser Ile
130 135 140

Thr Pro Asn Trp Thr Trp Phe Thr Ile Asp Tyr Ile Glu Val Ile His
145 150 155 160

Ala Pro Glu Pro Glu Asn His Asn Val Glu Lys Thr Leu Ile Asn Pro
165 170 175

Asn Ala Thr Asp Glu Ala Lys Ala Leu Ile Ser Tyr Leu Val Asp Asn
180 185 190

Phe Gly Glu Lys Ile Leu Ala Gly Gln His Asp Tyr Pro Asn Thr Arg
195 200 205

Pro Arg Asp Leu Glu Tyr Ile Tyr Glu Thr Thr Gly Lys Tyr Pro Ala
210 215 220

Val Leu Gly Leu Asp Phe Ile Asp Asn Ser Pro Ser Arg Val Glu Arg
225 230 235 240

Gly Ala Ser Ala Asp Glu Thr Pro Val Ala Ile Asp Trp Trp Asn Lys
245 250 255

Gly Gly Ile Val Thr Phe Thr Trp His Trp Asn Ala Pro Lys Asp Leu
260 265 270

Leu Asp Glu Pro Gly Asn Glu Trp Trp Ser Gly Phe Tyr Thr Arg Ala
275 280 285

Thr Thr Phe Asp Val Glu Tyr Ala Leu Lys His Pro Lys Ser Glu Asp
290 295 300

Tyr Met Leu Leu Ile Arg Asp Ile Asp Val Ile Ala Gly Glu Leu Lys
305 310 315 320

Lys Leu Gln Glu Ala Asn Val Pro Val Leu Trp Arg Pro Leu His Glu
325 330 335

Ala Glu Gly Gly Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Ser Thr
340 345 350

Lys Glu Leu Trp Arg Leu Met Tyr Asp Arg Met Thr Asn Tyr His Asn
355 360 365

Leu Asn Asn Leu Ile Trp Val Trp Asn Ser Ile Glu Glu Asp Trp Tyr
370 375 380

Pro Gly Asp Glu Tyr Val Asp Ile Val Ser Phe Asp Ser Tyr Pro Gly
385 390 395 400

Glu Tyr Asn Tyr Ser Pro Met Ser Arg Glu Tyr Glu Ala Leu Lys Glu
405 410 415

Leu Ser Ser Asn Lys Lys Leu Ile Ala Ile Ala Glu Asn Gly Pro Ile
420 425 430

Pro Asp Pro Asp Leu Leu Gln Leu Tyr His Ala Asn Tyr Ser Trp Phe
435 440 445

Ala Thr Trp Asn Gly Asp Ile Leu Arg Asn Gln Asn Ser Glu Glu His
450 455 460

Leu Arg Lys Val Tyr Asn His Asp Tyr Val Ile Thr Leu Asn Lys Leu
465 470 475 480

Pro Asn Leu Lys Thr Tyr Arg Gly Arg Cys Thr Tyr Thr Asp Thr Ile
485 490 495

<210> 29
<211> 1086
<212> DNA
<213> Bacillus licheniformis

41 248

e

<400> 29
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cagacggcat ctgctcatac agtgaatccg gtgaaccaa atgcccagtc gacaacgaag 120
gagctgatga attggcttgc tcatctgccg aaccgatcgg aaaatcgcg actgtcagg 180
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gaataa 1086

<210> 30
<211> 361
<212> PRT
<213> Bacillus licheniformis

<400> 30

Met Tyr Lys Lys Phe Gly Ile Ser Leu Leu Leu Ala Leu Leu Ile Val
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Ser Ala Phe Ser Gln Thr Ala Ser Ala His Thr Val Asn Pro Val Asn
20 25 30

Gln Asn Ala Gln Ser Thr Thr Lys Glu Leu Met Asn Trp Leu Ala His
35 40 45

Leu Pro Asn Arg Ser Glu Asn Arg Val Leu Ser Gly Ala Phe Gly Gly
50 55 60

Tyr Ser Asn Ala Thr Phe Ser Met Lys Glu Ala Asn Arg Ile Lys Asp
65 70 75 80

Ala Thr Gly Gln Ser Pro Val Val Tyr Ala Cys Asp Tyr Ser Arg Gly
85 90 95

Trp Leu Glu Thr Ala His Ile Ala Asp Ala Ile Asp Tyr Ser Cys Asn
100 105 110

Ser Asp Leu Ile Ser His Trp Lys Ser Gly Gly Ile Pro Gln Ile Ser
115 120 125

Met His Leu Pro Asn Pro Ala Phe Gln Ser Gly Asn Tyr Lys Thr Lys
130 135 140

Ile Ser Asn Ser Gln Tyr Glu Lys Ile Leu Asp Ser Ser Thr Thr Glu
145 150 155 160

Gly Lys Arg Leu Asp Ala Val Leu Ser Lys Val Ala Asp Gly Leu Gln
165 170 175

Gln Leu Lys Asn Glu Gly Val Pro Val Leu Phe Arg Pro Leu His Glu
180 185 190

Met Asn Gly Glu Trp Phe Trp Trp Gly Leu Thr Gly Tyr Asn Gln Lys
195 200 205

Asp Ser Glu Arg Ile Ser Leu Tyr Lys Gln Leu Tyr Gln Lys Ile Tyr
210 215 220

His Tyr Met Thr Asp Thr Arg Gly Leu Asp Asn Leu Ile Trp Val Tyr
225 230 235 240

Ala Pro Asp Ala Asn Arg Asp Phe Lys Thr Asp Phe Tyr Pro Gly Asp
245 250 255

Ser Tyr Val Asp Ile Val Gly Leu Asp Ala Tyr Phe Ser Asp Ala Tyr
260 265 270

Ser Ile Lys Gly Tyr Asp Glu Leu Thr Ala Leu Asn Lys Pro Phe Ala
275 280 285

Phe Thr Glu Val Gly Pro Gln Thr Thr Asn Gly Ser Leu Asp Tyr Ser
290 295 300

Gln Phe Ile Asn Ala Val Lys Gln Lys Tyr Pro Lys Thr Ile Tyr Phe
305 310 315 320

Leu Ala Trp Asp Glu Gly Trp Ser Pro Ala Ala Asn Gln Gly Ala Phe
325 330 335

Asn Leu Tyr Asn Asp Ser Trp Thr Leu Asn Lys Gly Glu Leu Trp Glu
340 345 350

Gly Ser Ser Leu Thr Pro Ala Ala Glu
355 360

<210> 31
<211> 3041
<212> DNA
<213> Caldocellulosiruptor sp.

<400> 31
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aatgtatcaa aaagggtgtca gtttctactg atttgcagcg acctggtaac aagtatgcgc 420
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 <212> PRT
 <213> Caldocellulosiruptor sp.

<400> 32

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20 25 30

Val Gln Ser Tyr Val Phe Asp Phe Glu Asp Gly Thr Thr Met Thr Phe
35 40 45

Gly Glu Ala Trp Gly Asp Ser Leu Lys Cys Ile Lys Lys Val Ser Val
50 55 60

Ser Thr Asp Leu Gln Arg Pro Gly Asn Lys Tyr Ala Leu Arg Leu Asp
65 70 75 80

Val Glu Phe Asn Glu Asn Asn Gly Trp Asp Gln Gly Asp Leu Gly Ala
85 90 95

Trp Ile Gly Gly Val Val Glu Gly Gln Phe Asp Phe Thr Asn Tyr Lys
100 105 110

Ser Val Glu Phe Glu Met Phe Val Pro Tyr Asp Glu Phe Ala Lys Ala
115 120 125

Lys Gly Gly Phe Ala Tyr Lys Val Val Leu Asn Asp Gly Trp Lys Glu
130 135 140

Leu Gly Ser Glu Phe Ser Ile Thr Val Asn Ala Gly Lys Lys Val Lys
145 150 155 160

Ile Asn Gly Lys Asp Tyr Met Val Ile His Lys Ala Phe Ala Ile Pro
165 170 175

Asp Asp Phe Arg Thr Lys Lys Arg Ala Gln Leu Val Phe Gln Phe Ala
180 185 190

Gly Gln Asn Cys Asn Tyr Lys Gly Pro Ile Tyr Leu Asp Asn Ile Arg
195 200 205

Val Arg Pro Glu Asp Ala Ser Asn Leu Ser Lys Glu Asp Tyr Gly Ser
210 215 220

Ser Glu Glu Glu Glu Ile Ser Glu Asp Phe Phe Thr Gly Val Thr Leu
225 230 235 240

Val Tyr Pro Gln Glu Gly Lys Asn Phe Val Tyr Asn Phe Glu Lys Asp
245 250 255

Thr Met Gly Phe Tyr Lys Tyr Ser Gly Asp Gly Phe Ala Lys Lys Thr
260 265 270

Lys Ser Met Glu Phe Ser Gln Asp Leu Lys Thr Ser Thr Asn Ala Gly
275 280 285

Ser Leu Lys Leu Asn Ala Asn Phe Gln Gly Thr Ala Phe Glu Glu Met
290 295 300

Asn Ile Ala Val Lys Leu Thr Asp Lys Glu Gly Lys Leu Phe Asp Leu
305 310 315 320

Gly Lys Tyr Ser Ala Leu Glu Tyr Thr Ile Tyr Ile Pro Asn Pro Asp
325 330 335

Lys Val Ala Gly Lys Ile Met Ser Ala Ser Ala Val Asp Ser Pro Trp
340 345 350

47 254

E

Lys Ile Ile Lys Asp Phe Thr Leu Leu Asn Tyr Lys Asp Lys Thr Thr
355 360 365

Trp Lys Glu Ile Asn Gly Lys Thr Tyr Ala Val Ile Lys Cys Lys Asp
370 375 380

Asn Leu Tyr Asn Val Lys Glu Lys Ala Gly Val Leu Val Leu Arg Ile
385 390 395 400

Ala Gly Ser Tyr Val Lys Tyr Thr Gly Pro Ile Tyr Ile Asp Asn Val
405 410 415

Thr Leu Ile Ala Gly Lys Lys Val Ala Pro Lys Val Glu Arg Ile Ser
420 425 430

Leu Pro Asn Pro Lys Thr Tyr Tyr Lys Val Lys Ile Glu Ala Glu Ser
435 440 445

Ala Ser Asp Gly Trp Ala Tyr Ser Val Glu Lys Glu Asn Ala Lys Phe
450 455 460

Ser Gly Lys Gly Tyr Val Leu Leu Phe Gly Asn Asn Met Gly Asn Thr
465 470 475 480

Leu Tyr Asn Ile Lys Val Pro Lys Thr Gly His Tyr Ile Phe Thr Leu
485 490 495

Ala Ile Ser Thr Leu Gly Leu Val Lys Asp Gly Ser Ile Asp Ile Trp
500 505 510

Ile Asp Gly Asp Leu Lys Gly Gly Ala Lys Val Pro Asn Val Lys Gly
515 520 525

Lys Phe Gln Glu Val Val Val Arg Lys Lys Ile Tyr Leu Thr Ala Gly
530 535 540

Glu His Thr Ile Ser Leu Gln Lys Ser Gly Gly Tyr Thr Ile Ala Val
545 550 555 560

Asp Tyr Phe Val Ile Glu Glu Leu Val Ala Ala Asn Lys Ser Lys Leu
565 570 575

Ser Val Ser Ser Lys Leu Val Thr Pro Asn Pro His Pro Asn Ala Gln
580 585 590

Arg Leu Ile Asn Tyr Leu Ser Ser Ile Tyr Gly Glu Lys Ile Leu Ser
595 600 605

Gly Gln Gln Ser Ser Gly Glu Gly Lys Glu Val Gln Met Ile Phe Asp
610 615 620

Val Thr Lys Arg Tyr Pro Ala Val Arg Ser Phe Asp Phe Met Asp Tyr
625 630 635 640

Ser Pro Ser Arg Val Gln His Gly Thr Lys Gly Thr Asp Val Asp Glu
645 650 655

Ala Ile Lys Trp Trp Lys Ser Gly Gly Ile Val Ala Phe Cys Trp His
660 665 670

Trp Asn Ala Pro Thr Gly Leu Ile Asp Gln Pro Gly Lys Glu Trp Trp
675 680 685

Arg Gly Phe Tyr Thr Glu Ala Thr Thr Phe Asp Leu Lys Lys Ala Met
690 695 700

Asp Asn Pro Asn Ser Glu Glu Tyr Lys Leu Ile Leu Arg Asp Ile Asp
705 710 715 720

Ala Ile Ala Glu Gln Leu Lys Lys Leu Gln Ala Glu Gly Val Pro Val
725 730 735

Leu Phe Arg Pro Leu His Glu Ala Ser Gly Gly Trp Phe Trp Trp Gly
740 745 750

Ala Lys Gly Pro Glu Pro Tyr Ile Lys Leu Trp Lys Leu Met Phe Asp
755 760 765

Arg Leu Val Asn Tyr His Lys Ile Asn Asn Leu Ile Trp Val Trp Asn
770 775 780

Gly Gln Asp Ala Ala Trp Tyr Pro Gly Asp Gln Tyr Val Asp Ile Ile
785 790 795 800

Ala Glu Asp Ile Tyr Glu Glu Lys Ala Gln Tyr Ser Pro Tyr Thr Glu

805

810

815

Arg Phe Val Lys Ala Leu Lys Tyr Thr Asn Ala Asn Lys Met Ile Ala
820 825 830

Leu Ser Glu Cys Gly Thr Ile Pro Asp Pro Ala Val Leu Lys Gln Glu
835 840 845

Gly Val Ser Trp Leu Trp Phe Ser Val Trp Ala Gly Ser Tyr Val Met
850 855 860

Thr Gly Ser Lys Tyr Asn Asp Glu Trp Asn Asp Asn His Met Leu Arg
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Ile Lys Ser Ile Pro Leu Lys
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<211> 1450

<212> RNA

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uuaaaagaug gcuccggcua ucacuacagg augggcccg gcgcgaauag cuaguuggua 180
agguaacggc uuaccaaggc gacgaugcgu agccgaccug agagggugau cggccacacu 240
gggacugaga cacggcccag acuccuacgg gaggcagcag uagggaaucu uccgcaaugg 300
acgaaagucu gacggagcaa cgccgcguga gcgaugaagg ccuucggguu guaaagcucu 360
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gcucaaccgg ggagggucau uggaacucgg gagacuugag uacagaagag gagaguggaa 600
uuccacgugu agcggugaaa ugcguagaua uguggaggaa caccaguggc gaaggcgacu 660
cucuggucug uaacugacgc ugaggcgca aagcgugggg agcaaacagg auuagauacc 720

50
257

E

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 <213> Bacillus sp. AAI12

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 acaucgaga aaucggugcu aaauaccgga aaucuuagag auugcauaa ccucuuguaa 180
 aagauggcuc cggcuauac uacggggaug gcccgcgcg cauuaagcuag uugguaaggu 240
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 aaccccgagc ggucauugga aacugggaga cuugaguaca gaagaggaga guggaaaucc 660
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<220>
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<210> 36
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<400> 36
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<210> 37
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<210> 38
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<220>
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<210> 39
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<210> 41
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45

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<220>

<223> Primer

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46

<210> 43

<211> 41

<212> DNA

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<223> Primer

<400> 43

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41

<210> 44

<211> 45

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<400> 44

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<210> 45

<211> 41

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<223> Primer

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<210> 47

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 47

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44

<210> 48

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 48

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49

<210> 49

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

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<210> 50

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

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<220>
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<210> 54
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